

84808

STIC-Biotech/Ch mLib

From: Kaushal, Sumesh
Sent: Tuesday, January 21, 2003 2:15 PM
To: STIC-Biotech/ChemLib
Subj ct: 09/734672 SEQ and Interference search

09/734672: SEQ and Interference search

Title: CODING SEQUENCES OF THE HUMAN BRCA1 GENE
Inventor: MURPHY, PATRICIA

Please search

SEQ ID NO:2
SEQ ID NO:4

thanks

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CREF

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 1/22
Date Completed: 1/23
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

☒ >gi|29725865|gb|AC134684.5| ☐ Homo sapiens chromosome 8, clone RP11-1118M6, complete sequence
Length = 175202

Score = 32.2 bits (16), Expect = . 14
Identities = 16/16 (100%)
Strand = Plus / Minus

Query: 6 acatgacagtgatact 21
|||||
Sbjct: 67785 acatgacagtgatact 67770

☒ >gi|24432075|ref|NM_145268.2| ☐ Homo sapiens LOC136263 (LOC136263), mRNA
Length = 1953

Score = 32.2 bits (16), Expect = 14
Identities = 16/16 (100%)
Strand = Plus / Plus

Query: 6 acatgacagtgatact 21
|||||
Sbjct: 459 acatgacagtgatact 474

☐ 1: [AC134684](#)

Homo sapiens chromosome 8, clone RP11-1118M6, complete sequence
gi|29725865|gb|AC134684.5|[29725865]

Links

☐ 2: [NM_145268](#)

Homo sapiens LOC136263 (LOC136263), mRNA
gi|24432075|ref|NM_145268.2|[24432075]

Links

☐ >[gi|30039658|gb|AY273801.1|](#) **LU** Homo sapiens breast cancer 1, early onset (BRCA1) gene, complete cds
Length = 82899

Score = 44.1 bits (22), Expect = 0.004
Identities = 25/26 (96%)
Strand = Plus / Plus

Query: 1 aaaagacatgacagtgatactttccc 26
 |||||
Sbjct: 32876 aaaagacatgacagcgatactttccc 32901

☐ >[gi|6552314|ref|NM_007302.1|](#) **LU** Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant
BRCA1-delta9-10, mRNA
Length = 6986

Score = 44.1 bits (22), Expect = 0.004
Identities = 25/26 (96%)
Strand = Plus / Plus

Query: 1 aaaagacatgacagtgatactttccc 26
 |||||
Sbjct: 2086 aaaagacatgacagcgatactttccc 2111

☐ >[gi|6552312|ref|NM_007301.1|](#) **LU** Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant
BRCA1-delta15-17, mRNA
Length = 6519

Score = 44.1 bits (22), Expect = 0.004
Identities = 25/26 (96%)
Strand = Plus / Plus

Query: 1 aaaagacatgacagtgatactttccc 26
 |||||
Sbjct: 2209 aaaagacatgacagcgatactttccc 2234

☐ >[gi|6552310|ref|NM_007300.1|](#) **LU** Homo sapiens breast cancer 1, early onset (BRCA1), transcript variant
BRCA1-delta14-18, mRNA
Length = 6313

Score = 44.1 bits (22), Expect = 0.004
Identities = 25/26 (96%)
Strand = Plus / Plus

Query: 1 aaaagacatgacagtgatactttccc 26
 |||||
Sbjct: 2209 aaaagacatgacagcgatactttccc 2234

BLASTN 2.2.6 [Apr-09-2003]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1055967163-024871-18415

Query=

(60 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)
1,801,791 sequences; 8,462,007,751 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Distribution of 103 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments

